Population genomics of *Mnemiopsis leidyi*, a notorious marine invader in the North Sea

Verwimp Christophe[1,2], Lies Vansteenbrugge[1], Lisa Devriese[1], Kris Hostens[1], Hilde Muylle[2], Olivier Honnay[3], Isabel Roldan-Ruiz[2], Tom Ruttink[2], and Johan Robbens[1]

[1] Animal Sciences Unit – Aquatic Environment and Quality, Institute for Agricultural and Fisheries Research (ILVO), Ankerstraat 1, 8400 Oostende, Belgium
E-mail: christophe.verwimp@ilvo.vlaanderen.be

[2] Plant Sciences Unit – Growth and Development, Institute for Agricultural and Fisheries Research (ILVO), Caritasstraat 21, B-9090 Melle, Belgium

[3] Evolution and Biodiversity Conservation Section, Department of Biology – Ecology, Katholieke Universiteit Leuven, Kasteelpark Arenberg 31, Box 2435, B-3001 Leuven, Belgium

The American comb jelly, *Mnemiopsis leidyi*, is an invasive species that is capable of endangering commercially important fishing grounds, through competition and predation. It gained significant attention in the scientific community following the depletion of anchovy stocks in the Black Sea in the '80s (Vinogradov *et al.*,1989). Since 2006, there were observations of this comb jelly in the Baltic Sea (Javidpour *et al.*, 2006) and the North Sea (Van Ginderdeuren *et al.*, 2012). In this project we investigate the populations of *M. leidyi* in the Belgian part of the North Sea (BPNS).

Next generation sequencing enables high resolution analyses of eukaryote genomes. An application of this technology, Genotyping-by-Sequencing (GBS), makes it possible to analyse genomes on a population-wide scale (Elshire *et al.*, 2011). During the first step of this project we will adapt GBS for *M. leidyi*. A critical aspect for this optimization is the choice of the restriction enzyme. Genomic differences, so-called Single Nucleotide Polymorphisms (SNPs), will be identified to discriminate individuals and to determine the relatedness to other individuals found at different locations or time periods.

In future steps of this project, we will develop a SNP marker set to resolve the population structure of *M. leidyi* in the BPNS. We will determine if and how they survive winter in this region and whether re-introduction through ballast water or migration from other seas occurs. This knowledge is essential for the development of effective control and mitigation measures.

References

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